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GenCore version 5.1.3
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OM protein - nucleic search, using frame_plus_p2n model

Run on: November 9, 2002, 04:42:12 ; Search time 69 seconds
(without alignments)
844.472 Million cell updates/sec

Title: US-09-895-298A-83
Perfect score: 1002
Sequence: 1 MMNRQPSKMRASQMMFF.....HDGSLDLRSRSVQEGNPRA 190

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 441362 segs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+g2n.model -DEV=xlp
-Q=/cg2_1/USPT0_spool/US09895298/runat_06112002_160416_2357/app.query.fasta.1.327
-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=rn1 -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NOR=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09895298.ecgn_1_1_31.ernat_06112002_160416_2357 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued_Patents_NA:*
1: /cg2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cg2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cg2_6/ptodata/1/ina/6A_COMB.seq:*
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5: /cg2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cg2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	88	8.8	4403765	4 US-09-103-840A-2	Sequence 2, Appl1
2	88	8.8	4411529	4 US-09-103-840A-1	Sequence 1, Appl1
3	86	8.6	1581	2 US-08-845-998-1	Sequence 1, Appl1
4	86	8.6	1581	3 US-09-206-537-1	Sequence 1, Appl1
5	86	8.6	1581	4 US-09-430-854-1	Sequence 1, Appl1
6	85	8.5	1168	4 US-08-858-207A-182	Sequence 182, App
7	82.5	8.2	40000	4 US-09-780-049-18	Sequence 18, Appl
8	80	8.0	2555	2 US-08-693-457-3	Sequence 3, Appl1
9	80	8.0	2555	4 US-09-265-731-3	Sequence 3, Appl1
10	79.5	7.9	450	4 US-09-235-451-11	Sequence 11, Appl
11	79	7.9	1491	4 US-09-134-001C-164	Sequence 164, App
12	78.5	7.8	1812	4 US-09-008-097-3	Sequence 3, Appl1

13	78.5	7.8	3549	4 US-09-008-097-5	Sequence 5, Appl1
14	78	7.8	2243	1 US-07-995-657-1	Sequence 1, Appl1
15	78	7.8	2243	1 US-08-474-587-1	Sequence 1, Appl1
16	78	7.8	10254	4 US-08-961-527-29	Sequence 29, Appl
17	77.5	7.7	4255	5 PCT-US96-02331-14	Sequence 14, Appl
18	77.5	7.7	4835	1 US-08-386-495-9	Sequence 9, Appl1
19	77.5	7.7	4835	5 PCT-US96-02331-9	Sequence 9, Appl1
20	77.5	7.7	7186	4 US-08-961-527-39	Sequence 39, Appl
21	77.5	7.7	8543	3 US-08-496-944-1	Sequence 1, Appl1
22	76.5	7.6	2713	4 US-08-285-439-1	Sequence 1, Appl1
23	76	7.6	4942	4 US-09-474-076-1	Sequence 1, Appl1
24	75.5	7.5	848	4 US-09-302-769-35	Sequence 35, Appl
25	75.5	7.5	939	4 US-09-134-001C-621	Sequence 621, App
26	75	7.5	1401	4 US-09-134-001C-183	Sequence 183, App
27	75	7.5	2352	2 US-08-889-909A-21	Sequence 21, Appl
28	75	7.5	2352	4 US-09-156-163A-21	Sequence 21, Appl
29	75	7.5	2602	4 US-08-838-151A-17	Sequence 17, Appl
30	75	7.5	4881	4 US-08-961-527-125	Sequence 125, App
31	75	7.5	16442	3 US-08-781-891-208	Sequence 208, App
32	74.5	7.4	893	1 US-08-276-452A-66	Sequence 66, Appl
33	74.5	7.4	893	2 US-08-798-744-66	Sequence 66, Appl
34	74	7.4	1209	4 US-08-791-115B-24	Sequence 24, Appl
35	74	7.4	1962	4 US-08-791-115B-3	Sequence 3, Appl1
36	74	7.4	3224	4 US-08-965-729A-2	Sequence 2, Appl1
37	73.5	7.3	1101	4 US-09-134-001C-2665	Sequence 2665, Ap
38	73.5	7.3	1239	4 US-09-134-001C-1112	Sequence 1112, Ap
39	73.5	7.3	2225	4 US-09-276-531-109	Sequence 109, App
40	73	7.3	1491	1 US-08-137-614A-3	Sequence 3, Appl1
41	73	7.3	1491	2 US-08-768-301-1	Sequence 1, Appl1
42	73	7.3	3518	4 US-09-412-210-2	Sequence 2, Appl1
43	72.5	7.2	2079	2 US-08-990-114-2	Sequence 2, Appl1
44	72.5	7.2	2079	4 US-09-241-333-2	Sequence 2, Appl1
45	72.5	7.2	3357	3 US-08-726-214-7	Sequence 7, Appl1

ALIGNMENTS

RESULT 1
US-09-103-840A-2
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Alignment Scores:

Pred. No.: 3.64e+04 Length: 4403765
Score: 88.00 Matches: 26
Percent Similarity: 47.62% Conservative: 14
Best Local Similarity: 30.95% Mismatches: 32
Query Match: 8.78% Indels: 12
DB: 4 Gaps: 4

US-09-895-298A-83 (1-190) x US-09-103-840A-2 (1-4403765)

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QY 6 ProProSerLysalaTrpArg-----AlaSerGlnmetMetThrPhePheIlePheLeu 23
      |||||
Db 207713 CCGCCGGGCGAGCGGTGGCGGTGTTATGCCGTTGTCTGCTCGGATTGACCATTCCTCTT 207772
QY 24 -----LeuphePheProSerPheThrGlyValLeuCysThrLeuAlaIle 38
      |||||
Db 207773 CTGGCCGTTAACCGGTTGTGTGTCGACGATACCGGATGGAGTCTTGCGCCGCTCTT 207832
QY 39 ThrIleTrpArgLeu-----LysProSerAlaAspCysGlyProPheArgGlyLeuPro 56
      |||||
Db 207833 ACCGGCATCCGGGTGGTTCGGCGTGCAGCGGCTCCGCATCGCTCGTGCGG----- 207883
QY 57 LeupheIleHisSerIleTyrSerTrpIleAspThrLeuSerThrArgProGlyTyrLeu 76
      |||||
Db 207884 TTGCTGTCCGGGATTTGGCGCAGCTGTGTGACACCCCTCTGCTGTTTGTGGGTTGGCTG 207943
QY 77 TrpValValTrp 80
      |||||
Db 207944 TGGCCGCTGTGG 207955
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RESULT 2
US-09-103-840A-1
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007-00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1
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Alignment Scores:
Pred. No.: 3.65e+04 Length: 4411529
Score: 88.00 Matches: 26
Percent Similarity: 47.62% Conservative: 14
Best Local Similarity: 30.95% Mismatches: 32
Query Match: 8.78% Indels: 12
DB: 4 Gaps: 4
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US-09-895-298A-83 (1-190) x US-09-103-840A-1 (1-4411529)

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QY 6 ProProSerLysalaTrpArg-----AlaSerGlnmetMetThrPhePheIlePheLeu 23
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QY 24 -----LeuphePheProSerPheThrGlyValLeuCysThrLeuAlaIle 38
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Db 207663 CTGGCCGTTAACCGGTTGTGTGTCGACGATACCGGATGGAGTCTTGCGCCGCTCTT 207722
QY 39 ThrIleTrpArgLeu-----LysProSerAlaAspCysGlyProPheArgGlyLeuPro 56
      |||||
Db 207723 ACCGGCATCCGGGTGGTTCGGCGTGCAGCGGCTCCGCATCGCTCGTGCGG----- 207773
QY 57 LeupheIleHisSerIleTyrSerTrpIleAspThrLeuSerThrArgProGlyTyrLeu 76
      |||||
Db 207774 TTGCTGTCCGGGATTTGGCGCAGCTGTGTGACACCCCTCTGCTGTTTGTGGGTTGGCTG 207833
QY 77 TrpValValTrp 80
      |||||
Db 207834 TGGCCGCTGTGG 207845
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RESULT 3
US-08-845-998-1/C
; Sequence 1, Application US/08845998
; Patent No. 5879892
; GENERAL INFORMATION:
; APPLICANT: Van Baren, Nicolas
; APPLICANT: Coulie, Pierre G.
; APPLICANT: De Smet, Charles
; APPLICANT: Lucas, Sophie
; APPLICANT: Boon, Thierry
; TITLE OF INVENTION: LEUKEMIA ASSOCIATED GENES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/845,998
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Van Amsterdam, John R.
; REGISTRATION NUMBER: 40,212
; REFERENCE/DOCKET NUMBER: L0461/7008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)720-3500
; TELEFAX: (617)720-2441
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1581 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 106..831
US-08-845-998-1
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Alignment Scores:
Pred. No.: 0.299 Length: 1581
Score: 86.00 Matches: 54
Percent Similarity: 39.92% Conservative: 41
Best Local Similarity: 22.69% Mismatches: 65
Query Match: 8.58% Indels: 78
DB: 2 Gaps: 16
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US-09-895-298A-83 (1-190) x US-08-845-998-1 (1-1581)

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QY 11 TrpArgAlaSerGlnmetMetThrPhePheIlePheLeuPhePheProSerPheThr 30
      |||||
Db 654 TTCAGCATCAGGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTT 595
QY 31 GlyVal---LeuCysThrLeuAlaIleThrIleTrpArgLeuLysProSerAlaAspCys 49
      |||||
Db 594 AGCCTGGGATCTCCAGCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 538
QY 50 -----GlyProPheArgGlyLeuProLeuPheIleHisSerIleTyrSerTrp 65
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QY 66 IleAsp-----ThrLeuSerThrArgProGlyTyrLeuTrp 77
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[illegible]

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1      RESULT 4
2      US-09-206-537-1/c
3      ; Sequence 1, Application US/09206537
4      ; Patent No. 6130052
5      ;
6      ; GENERAL INFORMATION:
7      ;
8      ; APPLICANT: Van Baren, Nicolas
9      ; APPLICANT: Coullie, Pierre G.
10     ; APPLICANT: De Smet, Charles
11     ; APPLICANT: Lucas, Sophie
12     ; APPLICANT: Boon, Thelery
13     ; TITLE OF INVENTION: LEUKEMIA ASSOCIATED GENES
14     ; NUMBER OF SEQUENCES: 16
15     ;
16     ; CORRESPONDENCE ADDRESS:
17     ; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
18     ; STREET: 600 Atlantic Avenue
19     ; CITY: Boston
20     ; STATE: MA
21     ; COUNTRY: US
22     ; ZIP: 02210
23     ;
24     ; COMPUTER READABLE FORM:
25     ; MEDIUM TYPE: Floppy disk
26     ; COMPUTER: IBM PC compatible
27     ; OPERATING SYSTEM: PC-DOS/MS-DOS
28     ; SOFTWARE: PatentIn Release #1.0, Version #1.25
29     ;
30     ; CURRENT APPLICATION DATA:
31     ; APPLICATION NUMBER: US/09/206,537
32     ; FILING DATE:
33     ; CLASSIFICATION:
34     ;
35     ; PRIOR APPLICATION DATA:
36     ; APPLICATION NUMBER: 08/845,998
37     ; FILING DATE:
38     ;
39     ; ATTORNEY/AGENT INFORMATION:
40     ; NAME: Van Amsterdam, John R.
41     ; REGISTRATION NUMBER: 40,212
42     ; REFERENCE/DOCKET NUMBER: L0461/7008
43     ; TELECOMMUNICATION INFORMATION:
44     ; TELEPHONE: (617)720-3500
45     ; TELEFAX: (617)720-2441
46     ;
47     ; INFORMATION FOR SEQ ID NO: 1:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 1581 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 106..831
US-09-206-537-1

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Alignment Scores:		
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Score:	86.00	54
Percent Similarity:	39.92%	41
Best Local Similarity:	22.69%	65
Query Match:	8.58%	78
DB:	3	16
	Gaps:	

US-09-895-298A-83 (1-190) X US-09-206-537-1 (1-1581)

[illegible]

Sequence 1, Application US/09430854
Patent No. 6271019
GENERAL INFORMATION:
APPLICANT: Van Baren, Nicolas
APPLICANT: Coulie, Pierre G.
APPLICANT: De Smet, Charles
APPLICANT: Lucas, Sophie
APPLICANT: Boon, Thierry
TITLE OF INVENTION: LEUKEMIA ASSOCIATED GENES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
STREET: 600 Atlantic Avenue
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/430,854
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/845,998
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Van Amsterdam, John R.
REGISTRATION NUMBER: 40,212
REFERENCE/DOCKET NUMBER: L0461/7008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)720-3500
TELEFAX: (617)720-2441
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1581 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 106..831
US-09-430-854-1
Alignment Scores:
Pred. No.: 0.299 Length: 1581
Score: 86.00 Matches: 54
Percent Similarity: 39.92% Conservative: 41
Best Local Similarity: 22.69% Mismatches: 65
Query Match: 8.58% Indels: 78
DB: 4 Gaps: 16
US-09-895-298A-83 (1-190) x US-09-430-854-1 (1-1581)
QY 11 TTPARGALASerGlnMetMetThrPhePheLeuLeuPhePheProSerPheThr 30
Db 654 TTCAGGCATCAGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTG 595
QY 31 G1YVal---LeuGysThrLeuAlaIleThrIleTrpArgLeuLysProSerAlaAspCys 49
Db 594 AGCCTGGGATCTGCCAGCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 538
QY 50 -----GlyProPheArgGlyLeuProLeuPheIleHisSerIleTyrSerTrp 65
Db 537 AAGCCAGGGGGAGGCGGCGGCGGAGATGCTGCCGCTT-----GTGCTGGGTTAC 490
QY 66 IleAsp-----ThrLeuSerThrArgProGlyTyrLeuTrp 77

Db 489 ATCCAGTACCATGAGCCATCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 442
QY 78 ValValTrpIleTyrArgAsnLeuIleGlySerValHis-----Phe 91
Db 441 -----TTTGTGGGGTCC--CACAGCCCCCTTCTCTCTCTCTCTCTCTCTCTCTCTCT 406
QY 92 PhePheIleLeuThrLeuIleValLeuIleIleThrTyrLeuTyrTrpGlnIleThrGlu 111
Db 405 CTCTCTCTCACACCT 349
QY 112 GlyArgLysIleMetIleArgLeuLeuHisGlnIleIleAsn----- 126
Db 348 GGAGAGCCAGTCAGATTGAAGATGCGACGCGGAGTGTCTCACCTCGTCCCTGCTTGCAG 289
QY 127 -----GluGlyLysAspLysMetPheLeuIleGlyLysLeuIleLys 140
Db 288 CCGCTGATGTTTCCCGGAGGAGAGAGAGGCGCTCTCACCTGCGCGCAGAGTATCAG 229
QY 141 LeuGlnAspMetGlyLys----- 147
Db 228 GCCCGAGTCTCCGCGCGCTGCT 169
QY 148 AlaAsnProSerSerLeuValLeuGluArgArgGluValGlnGln-----Gly 164
Db 168 GCCGGGACACCGGTCTGAGGTTCAGGTCAGAGCAGAGCAGACCAAGGCGCGG 109
QY 165 PheLeuHisLeuGly-----GluHisAspGlySer----- 174
Db 108 -----CATCGCGGCTCTGCGCAGAGTGGCTCCACAGATGGGTCCGGGATCCGGGGA 55
QY 175 LeuAspLeuArgSerArg-----ArgSerValGlnGlnGlyAsnProArgAla 190
Db 54 CTCGGAGTCCGAGTCGCGCAGTCAAGAGTCTGACGCTGAGACCCCGGCG 1
RESULT 6
US-08-858-207A-182/c
Sequence 182, Application US/08858207A
Patent No. 6348328
GENERAL INFORMATION:
APPLICANT: Black, Michael
APPLICANT: Hodgson, John
APPLICANT: Knowles, David
APPLICANT: Nicholas, Richard
APPLICANT: Stodola, Robert
TITLE OF INVENTION: No. 6348328e1 Compounds
NUMBER OF SEQUENCES: 552
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/858,207A
FILING DATE: 09-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/017670
FILING DATE: 14-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Glimm, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P50475
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090

TELEX:
; INFORMATION FOR SEQ ID NO: 182:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1168 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-858-207A-182

Alignment Scores:
Pred. No.: 0.252 Length: 1168
Score: 85.00 Matches: 39
Percent Similarity: 42.95% Conservative: 25
Best Local Similarity: 26.17% Mismatches: 48
Query Match: 8.48% Indels: 37
DB: Gaps: 7

US-09-895-298A-83 (1-190) x US-08-858-207A-182 (1-1168)

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Db 945 TTTCTTTACCTTCATTTTTCGCCAGTTCTTCCCTTCGTGACCGTAACAGACCGTTC 886
QY 34 CysThrleuAlaileThrileTrpArgleuLysProSerAlaaspCysglyProPheArg 53
::: ::| ||| ||| ||| |||
Db 885 AAGAGTTCTGGGTGGTATTCACAGAGTTCCATTCATTTCTTCTTGTTC--- 829
QY 54 GlyleuProleuPheileHisserileTyrserTrpileAspThrleuSerThrArgPro 73
||| ||||| :||| ||||| |||
Db 828 ---TTAGAGTTGTTT-----GAGATGACAAAGTTAGCAACT----- 796
QY 74 GlyTyrleuTrpValValTrpileTyrArgAsnleuileGlySerValHisPhePhe 93
||||||| ||||| |||||
Db 795 -----TGCTGTGTTTG-----TTTTC 778
QY 94 IleleuThrleuileValleuilelele-ThrTyrleuTyrTrpGlnleThrGluGly-- 112
:||||| :||||| ||||| |||||
Db 777 TTGATGAGATGATGATGTTGATTTGATATCTTGTGCAACACGTCGAAAGCAAG 718
QY 113 -----ArglysileMetileArgleuileHisGlu-----GlnleileAsnGln 127
:||||| :||||| ||||| |||||
Db 717 CTGTACCGTAGTCAGCGTGTCTGTCTTCTTACGACGACGACGATATCTTGTGTA 658
QY 127 uGlyLysAspLysMetPheleuileGluLysleuileLysleuGlnAspMetGluLysly 147
||||| ||| ||| ||| ||| |||
Db 657 AGGTCAAGAGATCGCTTGTTCGACGCTTTTGAATGTAGCCACGCTTCAATGAAT 598
QY 147 SALAsnProSerSerleuValleu 155
||||| |||||
Db 597 TTGTGAAGAGTCTTCAAGTGTCTT 573

US-09-780-049-18

Sequence 18, Application US/09780049

Patent No. 6465250

GENERAL INFORMATION:

APPLICANT: Brett P. Monia

APPLICANT: Jacqueline Wyatt

TITLE OF INVENTION: ANTISENSE MODULATION OF PROTEIN PHOSPHATASE 2 CATALYTIC SUBUNIT

TITLE OF INVENTION: EXPRESSION

FILE REFERENCE: RFS-0134

CURRENT APPLICATION NUMBER: US/09/780,049

CURRENT FILING DATE: 2001-02-09

NUMBER OF SEQ ID NOS: 96

SEQ ID NO 18

LENGTH: 40000

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

US-09-780-049-18

Alignment Scores: 128 Length: 40000
Pred. No.: 128

Score: 82.50 Matches: 29
Percent Similarity: 41.90% Conservative: 15
Best Local Similarity: 27.62% Mismatches: 34
Query Match: 8.23% Indels: 27
DB: Gaps: 4

US-09-895-298A-83 (1-190) x US-09-780-049-18 (1-40000)

QY 23 LeuLeuPhePheProSerPheThrGlyValleuCysThrleuAlaileThrileTrpArg 42
|||||||:| ||| |||||:|
Db 18087 TTATGTTCTACTGTTCT-----GGTGTAGCTGTATTATGTTGTAATACTATCTGAGAG 18140
QY 43 Leu-----LysProSerAlaaspCysgly 50
||| ||| |||
Db 18141 CTGTTAAGTTGAGACCAAAACAAACAAACAAACAAACAAATCATGCTTAAACTGCT 18200
QY 51 ProPheArgGly---LeuProleuPheileHisserileTyrserTrpileAspThrleu 69
|||||:| ||| |||||:|
Db 18201 TCTTCCAAAGTTGCATTTTGTTAAGATCTACTTAATAGTTGATTTGATGATTTT 18260,
QY 70 SerThrArgProGlyTyrleuTrpValValTrpileTyrArgAsnleuileGlySerVal 89
||| ||| ||| ||| ||| |||
Db 18261 TCCCCCTCCGCTGAGGATGTTGCTTACTGTATACCACTGTATCGCCAGT--- 18317
QY 90 HisPhePhePheileleuThrleuileValleuileleThrTyrleuTyrTrpGlnle 109
||| ||| ||| ||| ||| |||
Db 18318 -----ATTTAATATATTTGTTCTGCTGCTGTG 18344
QY 110 ThrGluGlyArgLys 114
|||||||
Db 18345 AAGTTGCTAGGAAG 18359

RESULT 8

US-08-693-457-3/c

Sequence 3, Application US/08693457

Patent No. 5880330

GENERAL INFORMATION:

APPLICANT: Weigel et al., Detlef

TITLE OF INVENTION: SHOOT MERISTEM SPECIFIC PROMOTER

TITLE OF INVENTION: SEQUENCES

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.

STREET: 4225 Executive Square, Suite 1400

CITY: La Jolla

STATE: CA

COUNTRY: USA

ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/693,457

FILING DATE: 07-AUG-1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Haile, Lisa A.

REGISTRATION NUMBER: 38,347

REFERENCE/DOCKET NUMBER: 07251/012001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 619/678-5070

TELEFAX: 619/678-5099

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 2555 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-693-457-3

Alignment Scores:


```

QY 111 G|U|G|Y|A|R|G|I|L|E|I|E|A|R|G|L|E|U|H|I|S|G|L|U|I|I|E|I|E|A|S|N|G|U|G|Y|L|Y|S|--- 129
      ::||| |||:::|||||::: ||| ||| |||
Db 1161 A|A|T|A|T|A|A|A|A|A|G|A|A|A|A|T|A|A|A|T|T|A|C|T|A|A|C|T|A|C|A|A|A|A|A|T|A|T|T|T|T|A|T|A|A|A|A|T|A 1102
      ::||| |||:::|||||::: ||| ||| |||
QY 130 A|S|P|L|Y|S|E|T|P|H|E|U|I|E|C|L|U|L|Y|S|E|U|I|E|L|Y|S|L|E|U|G|I|N|A|S|P|E|T|G|L|U|L|Y|S|L|A|A|S|N 149
      ::||| ||| ||| |||::: ||| ||| |||
Db 1101 G|A|A|A|C|A|T|A|T|T|T|T|T|A|T|T|T|C|T|A|T|C|T|A|A|A|T|C|C|A|A|A|A|C|A|C|A|T|C|A|A|A|T|A|A|A|G|A|G|A|N|C 1042
      ::||| ||| ||| |||::: ||| ||| |||
QY 150 P|R|O|S|E|R|S|E|U|E|V|A|L|E|U|G|I|N 156
      |||:::|||||:::
Db 1041 A|T|A|G|T|G|A|G|T|A|T|G|G|T|T|T|A|A|A 1021

```

```

RESULT 10
US-09-235-451-11
; Sequence 11, Application US/09235451
; GENERAL INFORMATION:
; APPLICANT: Juliana, David J.
; APPLICANT: Caterina, Michael J.
; APPLICANT: Brake, Anthony J.
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES ENCODING
; TITLE OF INVENTION: CAPSAICIN RECEPTOR AND CAPSAICIN RECEPTOR-RELATED
; FILE REFERENCE: 9076/084CIP
; CURRENT APPLICATION NUMBER: US/09/235,451
; CURRENT FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/072,151
; PRIOR FILING DATE: 1998-01-22
; PRIOR APPLICATION NUMBER: 08/915,461
; PRIOR FILING DATE: 1997-08-20
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 450
; TYPE: DNA
; ORGANISM: M. musculus
US-09-235-451-11

```

Alignment Scores:	
Pred. No.:	0.294
Score:	79.50
Percent Similarity:	44.37%
Best Local Similarity:	28.17%
Query Match:	7.93%
DB:	4
Length:	450
Matches:	40
Conservative:	23
Mismatches:	63
Indels:	16
Gaps:	6

US-09-895-298A-83 (1-190) x US-09-235-451-11 (1-450)

[illegible]

Db	345	GCTGGGGTTCACCGCCGACGGCAGATGACTTCGCGTGTCCTCAAGGGTGATGAGGT	404
Qy	186	YAsn	187
Db	405	GAAC	408

```

RESULT 11
US-09-134-001C-164
; Sequence 164, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 164
; LENGTH: 1491
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-164

```

Alignment scores:	
Pred. No.:	2.19
Score:	79.00
Matches:	37
Percent Similarity:	79.63%
Conservative:	28
Best Local Similarity:	22.56%
Mismatches:	45
Query Match:	7.88%
DB:	4
Gaps:	8

US-09-895-298A-83 (1-190) x US-09-134-001C-164 (1-1491)

OY	27	ProserPheThrGlyValLeuCysThrLeuAlaIleThrIleTrpArgLeuLysProSer	46
		::::: :::	
Db	553	CCTATATTCTAGTATTATATGCATGATAGTGCACTTACAACTTCAGTACTTTAATACC	612
OY	47	AlaAspCysGlyProPheArgGlyLeuProLeuPheIleHisSerIleTyrSerTrpIle	66
		:::	
Db	613	GGT-----TTTATGCGTATGACTAGTGGAGAAGTGTGGCGTTTTTACTGTGGGA	660
OY	67	AspThrLeuSer----ThrArgProGlyTyrLeuTrpValValTripletYrrArgAsnLeu	85
		:::~::~ :::~::~ :	:
Db	661	GATACAATGGCACACAGTAATAAAGTACTATGTTAGTAACGTATGGGTATTCACAGGAGATT	720
OY	86	IleGlySerValHisPhe-----PhePhe	93
		:::~::~	
Db	721	GAGGAGCCGTTGTCTTTTCTCGGACGTGCACAAAGTCTAAAAAGATGTAGGAACCTCTACC	780
OY	94	IleLeuThrLeuIle--ValLeuIleIleThrTyrLeuTyrTrpGlnIleThrGluGly	112
		:::~::~ :::~::~ : :::	:
Db	781	GTTATTGGTTGATTCTGTGCTAGTCACTTTATTCTTAATGACTGTACTAGCCCCAAGGT	840
OY	113	ArgGlyIleMetIleArgLeuLeuHisGluGlnIleIleAsnGluGlyLysAspLysMet	132
		:::~::~ :::~::~ :::~::~	
Db	841	-----GTCATTCACCACGAAACCAAATTCCA-----	864
OY	133	PheLeuIleGluLysLeuIleLysLeuGlnAspMetGluLysLysAlaAsnProSer---	151
Db	865	-----AAACTTGCTAATCCATCAATG	885
OY	152	SerLeuValLeuGluArgArgGluValGluGlnGlnGlyPheLeuHisLeuGlyGluHis	171
		::: :::	
Db	886	GCACAAGATATTAGAA-----CATATTGTAGTGCAT	915
OY	172	AspGlySerLeu 175	
		:::	
Db	916	TGGGGTTCAGTG 927	

RESULT 12
US-09-008-097-3
; Sequence 3, Application US/09008097
; Patent No. 6306830
; GENERAL INFORMATION:
; APPLICANT: Hammond, H. Kirk
; APPLICANT: Insel, Paul A.
; APPLICANT: Ping, Peipei
; APPLICANT: Post, Steven R.
; APPLICANT: Gao, Meihua
; TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE
; TITLE OF INVENTION: HEART FAILURE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESS: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/008,097
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Dylan, Tyler M
; REGISTRATION NUMBER: 37,612
; REFERENCE/DOCKET NUMBER: 22000-20567.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-813-5600
; TELEFAX: 650-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1812 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1..1812
; OTHER INFORMATION:
; US-09-008-097-3

Alignment Scores:
Pred. No.: 3.45 Length: 1812
Score: 78.50 Matches: 42
Percent Similarity: 40.33% Conservative: 31
Best Local Similarity: 23.20% Mismatches: 63
Query Match: 7.83% Indels: 45
DB: 4 Gaps: 8

US-09-895-298A-83 (1-190) x US-09-008-097-3 (1-1812)
QY 30 ThrglyValLeuGcsthrLeuAlaIlethrIletrpArgLeuLysProSer---AlaAs 48
DB 83 TCTGTGCCCCGTGTGTTCTTTGTATACATCGCATACAGCTCTCCCGCATCGCGGG 142
QY 48 pcysglyPropheargGlyLeuProLeuphe-IleHisSerIleTyrSertrpIleAspt 68
DB 143 CTGCGCTCTCAGCGGCTGGGCTCCACCTTCGATTTGATCTTGCGCTG-----C 196
* QY 68 hrLeuSerThrArgProGlyTyrIleuTrpValValtrpIleTyrArgAsnLeuIleGlyS 88
||||:| :|||

DB 197 AACTTAACCGTGTGATGCGCTTCTCTGTG-----AAGCAGCTCGGTG 238
QY 88 ervaIHisphethepheIleLeuThrLeuIleValLeuIleIleThrTyrLeuTyrTrpG 108
DB 239 CCAATGTGCTGTGTCTCTCTGCACCAACGTCATATGATCTGCACACACTATCCAGCAG 298
QY 108 InIlethr-----GluGlyArgLysIleMetIleArgLeuLeuHisG 122
DB 299 AGGTGCTCAGCGCCAGCGCTTTCAGAGACCCGAGTTACATCCAGCCCGGCTCCACC 358
QY 122 IuGlnIleIleAsnGluGlyLysAspLysMetPheLeuIleGluLysLeuIleLysLeuG 142
DB 359 TGCAGCATGAGAAATCGGACGACGAGCGGCTGCTGTG----- 396
QY 142 InAspMetGluLysLysAlaAsnProSerSerLeuValLeuGluArgArgGlu----- 159
DB 397 -----TCGGTATTGCCCGCCAGACGTTGCCATGAGATGAAGAAGACATCA 442
QY 160 --ValGluGlnGlnGlyPheLeuHis-----LeuGlyGluHisAsp----- 172
DB 443 ACACAAAAAAGAAAGACATGTTCCACAAAGATCTACATACAGAGCATGCAATGTCAGCA 502
QY 173 -----GlySerLeuAspLeuArgSerArgArgSerValGlnGlu 185
DB 503 TCCTGTTTGCAGACATTTAGGGCTTCCACCAGCCTGGCATCCAGTGCACCTGCCAGGAG 561

RESULT 13
US-09-008-097-5
; Sequence 5, Application US/09008097
; Patent No. 6306830
; GENERAL INFORMATION:
; APPLICANT: Hammond, H. Kirk
; APPLICANT: Insel, Paul A.
; APPLICANT: Ping, Peipei
; APPLICANT: Post, Steven R.
; APPLICANT: Gao, Meihua
; TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE
; TITLE OF INVENTION: HEART FAILURE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESS: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/008,097
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Dylan, Tyler M
; REGISTRATION NUMBER: 37,612
; REFERENCE/DOCKET NUMBER: 22000-20567.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-813-5600
; TELEFAX: 650-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3549 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:

```
; NAME/KEY: Coding Sequence
; LOCATION: 1...3501
; OTHER INFORMATION:
US-09-008-097-5

Alignment Scores:
Pred. No.: 9.8 Length: 3549
Score: 78.50 Matches: 42
Percent Similarity: 40.33% Conservative: 31
Best Local Similarity: 23.20% Mismatches: 63
Query Match: 7.83% Indels: 45
DB: 4 Gaps: 8

US-09-895-298a-83 (1-190) x US-09-008-097-5 (1-3549)

QY 30 ThrGlyValLeuGysThrLeuAlaIleThrIleTrpArgLeuLysProSer-----Alaas 48
DB 716 TCTGTGTCCTGCTGTTCTTGTATACATGCGATACACGCTCCCTCCCATCCGATGCGGG 775
QY 48 pCysGlyProPheArgGlyLeuProLeuPhe-IleHisSerIleTyrSerTrpIleAsp 68
DB 776 CTGCCGTCCTCAGCGGGCTGGGCTCTCCACCTTGATTTGATCTTGCGCTGG-----C 829
QY 68 hIleuSerThrArgProGlyTyrLeuTrpValValTrpIleTyrArgAsnLeuIleGly 88
DB 830 AACTTAACCGTGTGATGCTTCCTCTG-----AAGCAGCTCGGTG 871
QY 88 erValHisPhePheIleLeuThrLeuIleValLeuIleIleThrTyrLeuTyrTrp 108
DB 872 CCAATGTGCTGCTGTTCTCTGCGACCAACGTATTAGCATCTGCACACACTATCCAGCAG 931
QY 108 InIleThr-----GluGlyArgLysIleMetIleArgLeuLeuHis 122
DB 932 AGGTGCTCTCAGCGCCGAGGCTTTCAGGAGACCCGCGATTACATCCAGGCCCGGCTCCACC 991
QY 122 LuGlnIleIleAsnGluGlyLysAspLysMetPheLeuIleGluLysLeuIleLysLeu 142
DB 992 TGCAGCATGAGAAATCGCGACAGAGCGGCTGCTG----- 1029
QY 142 InAspMetGluLysLysAlaAsnProSerSerLeuValLeuGluArgArgGlu----- 159
DB 1030 -----TCGGTATTGCCCCACAGCAGCTGCCATGAGATGAAGAAGACATCA 1075
QY 160 --ValGluGlnGlnGlyPheLeuHis-----LeuGlyGluHisAsp----- 172
DB 1076 ACACAAAAAAGAGAAGACATGTTCCACAAAGATCTACATFACAGAAAGCATGACATGCAGCA 1135
QY 173 -----GlySerLeuAspLeuArgSerArgArgSerValGlnGlu 185
DB 1136 TCCTGTTTGAGACATGAGGCTTCACACAGCTGCATCCAGTGCACCTGCGCAGAG 1194

RESULT 14
US-07-995-657-1
; Sequence 1, Application US/07995657
; Patent No. 5443974
; GENERAL INFORMATION:
; APPLICANT: Hitz, William D.
; APPLICANT: Yadav, Narendra S.
; APPLICANT: Perez_Grau, Luis
; TITLE OF INVENTION: Nucleotide Sequence of
; TITLE OF INVENTION: Soybean Stearoyl-ACP
; TITLE OF INVENTION: Desaturase cDNA
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. du Pont de Nemours
; ADDRESSEE: and Company
; STREET: 1007 Market Street
; CITY: Wilmington
; STATE: Delaware
; COUNTRY: U.S.A.
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB
```

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COMPUTER: Macintosh
OPERATING SYSTEM: Macintosh System, 6.0
SOFTWARE: Microsoft Word, 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/995,657
FILING DATE: 19921211
FILING DATE: C) CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: GEIGER, KATHLEEN W.
REGISTRATION NUMBER: 35,880
REFERENCE/DOCKET NUMBER: BB_1022-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-892-8112
TELEFAX: 302-892-7949
TELEX: 835420
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2243 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Glycine max
STRAIN: Cultivar Wye
DEVELOPMENTAL STAGE: Developing seeds
IMMEDIATE SOURCE:
LIBRARY: cDNA to mRNA
CLONE: pDS1
FEATURE:
NAME/KEY: 5' non-coding sequence
LOCATION: 1..69
OTHER INFORMATION: /note="IDENTIFICATION
OTHER INFORMATION: METHOD-Deduced by proximity to location 70-72"
FEATURE:
NAME/KEY: Putative translation initiation codon
LOCATION: 70..72
OTHER INFORMATION: /note="IDENTIFICATION
OTHER INFORMATION: METHOD-Similarity of the context of the
OTHER INFORMATION: methionine codon in the open reading frame to
OTHER INFORMATION: translation
FEATURE:
NAME/KEY: Putative transit peptide coding sequence
LOCATION: 70..165
OTHER INFORMATION: /note="IDENTIFICATION
OTHER INFORMATION: METHOD-Deduced by proximity to location 70-72
OTHER INFORMATION: and location 166-1242"
FEATURE:
NAME/KEY: Mature protein coding sequence
LOCATION: 166..1242
OTHER INFORMATION: /note="IDENTIFICATION
OTHER INFORMATION: METHOD-Experimental determination of N-terminal
OTHER INFORMATION: amino acid sequence and subunit size of
OTHER INFORMATION: purified soybean
FEATURE:
NAME/KEY: Translation termination codon
LOCATION: 1243..1245
OTHER INFORMATION: /note="IDENTIFICATION
OTHER INFORMATION: METHOD-The translation codon ends the open
OTHER INFORMATION: reading frame for a protein of the expected
OTHER INFORMATION: size"
FEATURE:
NAME/KEY: 3' non-coding sequence
LOCATION: 1246..2243
OTHER INFORMATION: /note="IDENTIFICATION
OTHER INFORMATION: METHOD-Established by proximity to location
OTHER INFORMATION: 1243-1245"
US-07-995-657-1
```



```
; FEATURE:
; NAME/KEY: 3' non-coding sequence
; LOCATION: 1246..2243
; OTHER INFORMATION: /note="IDENTIFICATION
; OTHER INFORMATION: METHOD=Established by
; OTHER INFORMATION: proximity to location
; OTHER INFORMATION: 1243-1245"
US-08-474-587-1
```

```
Alignment Scores:
Pred. No.: 5.57 Length: 2243
Score: 78.00 Matches: 43
Percent Similarity: 34.63% Conservative: 28
Best Local Similarity: 20.98% Mismatches: 56
Query Match: 7.78% Indels: 78
DB: 1 Gaps: 9
```

US-09-895-298a-83 (1-190) x US-08-474-587-1 (1-2243)

```
QY 19 PhePheIlePheLeuLeuPhePheProSerPheThrGlyValLeuCysThrLeu----- 36
    ||| |||||::: ||||| ||| |||||:::
DB 1324 TTGTGATTTTATCTTTTCTTCTCCTGTTTTC--GTCCTATGTATATGCCACTG 1380

QY 37 -----AlaIleThrIleTrp-----Arg 42
    ::: |||
DB 1381 TAAGGTGAACAGTTGTTCTGCAATGTCGCAAGTTAAGCAGTTAGGGCAGCTGAGT 1440

QY 43 LeuLysProSerAlaAspCysGlyProPheArgGlyLeuProLeuPheIleHisSerIle 62
    ::::: ::: ||| |||||
DB 1441 ATTAGAAATGCTATTGTTGTTCCCTTT----- 1470

QY 63 TyrSerTrpIleAspTrpIleuSerThrArgProGlyTyrLeuTrp-----ValValTrp 80
    ||||| ||||| ::: |||
DB 1471 -----CTGTGGTAGTGATGTCGTGG 1491

QY 81 IleTyrArgAsnLeuIleGlySerValHisPhePheIleLeuThrLeuIleValLeu 100
    ||::: ||||| ||| :::::
DB 1492 AAGTATTAAGTAAACG-----TTTCTCTGCAATTTTGTGATGATA 1536

QY 101 IleIleThrTyrLeuTyrTrpGlnIleThrGlnGlyArgLysIle----- 115
    ::: |||||
DB 1537 -----AAGAAATTTAGTTCTAATAAACCG 1560

QY 116 -----MetIleArgLeuLeuHisGlnIle 124
    :::
DB 1561 TCGCACCCTCCCTGAGGCTTCTGTCTGTCGCGAGTGACCATGGTGAGGGTTAGTGTG 1620

QY 125 IleAsnGlnGlyLysAspLysMetPheLeuIleGlnLysLeuIleLysLeuGlnAspMet 144
    ::: ||::: ||||| ||| ||| |||
DB 1621 CTGAACGATGCTCTGAAGAGCATGTACAAATGCTGAGAAAGGGGAAAGGCCCAAGTCATG 1680

QY 145 GlnLysLysAlaAsnProSerSerLeuValLeuGlnArgGlnValGlnGlnGlnGly 164
    ||||| ||||| ::: |||
DB 1681 -----ATTGGGCCATTCCTCCAAAGTCATTAATTCCTTTGGTGATGCAGAAG 1731

QY 165 PheLeuHisLeuGlnHisAspGlySerLeuAspLeuArgSerArgArgSerValGln 184
    ::: ||||| ::: ||| ||:::
DB 1732 CACGGATACATGGAGATTGTGATGATGATGACACAGGCGTGTAAATCGTGGTT 1791

QY 185 GlnGlyAsnProArg 189
    ||| ||| |||
DB 1792 GAATTGAACGGTAGA 1806
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Search completed: November 9, 2002, 06:47:48
Job time : 2124 secs

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